What is claimed is:

1. A method of identifying a pathogen in a biological sample comprising the steps of:

amplifying at least one nucleic acid molecule obtained from a biological sample with at least one pair of intelligent primers to obtain at least one amplification product; and

determining the molecular mass of the at least one amplification product wherein said molecular mass identifies the pathogen in the biological sample.

2. A method of claim 1 wherein the pathogen is a bacterium, a virus, a parasite, or a fungus.

3. A method of claim 1 wherein the biological sample is blood, mucus, hair, urine, breath, stool, or tissue biopsy.

4. A method of claim 1 wherein the biological sample is obtained from an animal.

5. A method of claim 4 wherein the animal is a human.

6. A method of claim 1 wherein the molecular mass is determined by mass spectrometry.

7. A method of claim 6 wherein the mass spectrometry is Fourier transform ion cyclotron resonance mass spectrometry (FTICR- MS), ion trap, quadrupole, magnetic sector, time of flight (TOF), Q-TOF, or triple quadrupole.

8. A method of claim 1 wherein the intelligent primers are targeted to ribosomal RNA or housekeeping genes.

9. A method of claim 1 wherein the molecular mass is used to determine the base composition of said amplification product and wherein said base composition identifies said pathogen.

10. A method of identifying a pathogen in a biological sample comprising the steps of:

amplifying at least one nucleic acid molecule obtained from a biological sample

with at least one pair of intelligent primers to obtain at least one amplification product;

digesting at least one amplification product with restriction enzymes to produce a plurality of restriction digest products; and

determining the molecular mass of at least one restriction digest product; wherein the molecular mass identifies the pathogen in the biological sample.

11. The method of claim 10 wherein said molecular mass is used to determine the base composition of said restriction digest product and wherein said base composition identifies said pathogen.

12. A method of identifying a plurality of etiologic agents of disease in an individual comprising the steps of:

amplifying at least one nucleic acid molecule obtained from a biological sample from the individual with a plurality of intelligent primers to obtain a plurality of amplification products corresponding to the plurality of etiologic agents; and

determining the molecular masses of the plurality of amplification products; wherein the molecular masses identify the plurality of etiologic agents.

13. A method of claim 12 wherein the etiologic agents are bacteria, viruses, parasites, or fungi, or any combination thereof.

14. A method of claim 12 wherein the biological sample is blood, mucus, hair, urine, breath, stool, or tissue biopsy.

15. A method of claim 12 wherein the biological sample is obtained from an animal.

16. A method of claim 15 wherein the animal is a human.

17. A method of claim 12 wherein the molecular mass is determined by mass spectrometry.

18. A method of claim 17 wherein the mass spectrometry is Fourier transform ion cyclotron resonance mass spectrometry (FTICR- MS), ion trap, quadrupole, magnetic sector,

time of flight (TOF), Q-TOF, or triple quadrupole.

19. A method of claim 12 wherein the molecular masses are used to determine the base composition of the amplification products and wherein the base compositions identify the pathogen.

20. A method of *in silico* screening of intelligent primer sets for identification of a plurality of bioagents comprising the steps of:

preparing a base composition probability cloud plot from a plurality of base composition signatures of the plurality of bioagents generated in silico;

inspecting the base composition probability cloud plot for overlap of clouds from different bioagents; and

selecting primer sets based on minimal overlap of the clouds.

21. A method of predicting the identity of a bioagent having a heretofore unknown base composition signature comprising the steps of:

preparing a base composition probability cloud plot from a plurality of base composition signatures of known bioagents and the heretofore unknown base composition;

inspecting the base composition probability cloud for overlap of the heretofore unknown base composition with the cloud of a known bioagent, wherein overlap predicts that the identity of the bioagent with a heretofore unknown base composition signature is the known bioagent.

22. A method of claim 21 wherein the heretofore unknown base composition signature is entered into a database of base composition signatures and is included in subsequent analyses comprising the base composition probability cloud of the known bioagent.